SEQUENCE LISTING 28 MAR 2006

<110>	BIOAXONE THERAPEUTIQUE	INC.
	MCKERRACHER, LISA	
	LASKO, DANA	

- <120> COMPOSITIONS AND METHODS FOR TREATING TUMOR SPREADING
- <130> 16627-2PCT
- <150> US 10/902,879
- <151> 2004-08-02
- <150> US 60/506,162
- <151> 2003-09-29
- <160> 59
- <170> PatentIn version 3.1
- <210> 1
- <211> 27
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Oligonucleotide used to remove the stop codon from ADP-ribosyl tr ansferase C3 (Clostridium botulinum) cDNA.

PCT/CA2004/001763

WO 2005/030248

<400> 1

gaattcttta ggattgatag ctgtgcc

27

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- <213> Artificial Sequence
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- <223> Oligonucleotide used to remove the stop codon from ADP-ribosyl tr ansferase C3 (Clostridium botulinum) cDNA.
- <400> 2

ggtggcgacc atcctccaaa a

. 21

- <210> 3
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- <212>
- <213> Artificial Sequence
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- Sequence of C3APL: includes ADP-ribosyl transferase C3 (Clostrid <223> ium botulinum) and Antennapedia sequence.
- <220>
- <221> CDS
- <222> (1)..(888)

336

<223>

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Gly	Ser	Ser	Arg	Val	Asp	Leu	Gln	Ala	Сув	Asn	Ala	Tyr	Ser	Ile _.	Asn ·	
1				5					10					15		
caa	aag	gct	tat	tca	aat	act	tac	cag	gag	ttt	act	aat	att	gat	caa	96
Gln	Lys	Ala	Tyr	Ser	Asn	Thr	Tyr	Gln	Glu	Phe	Thr	Asn	Ile	Ąsp	Gln	
			20					25					30			
gca	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	144
Ala	Lys	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	ГЛЗ	Tyr	Gly	Leu	Ser	Lys	
	:	35					40					45				
											•			`		
tca	gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt.	gaa	ata	192
Ser	Glu	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile	
	50	•				55					60					
aat	gga	aag	cta	aga	.caa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca	240
Ąsn	Gly	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	
65					70					.75				•	80	•
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	
				85					90					95		

aag acc cct gaa aat att atg tta ttt aga ggc gac gac cct gct tat

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr tta gga aca gaa ttt caa aac act ctt ctt aat tca aat ggt aca att Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile aat aaa acg gct ttt gaa aag gct aaa gct aag ttt tta aat aaa gat Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 13.0 aga ctt gaa tat gga tat att agt act tca tta atg aat gtc tct caa Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln ttt gca gga aga cca att att aca caa ttt aaa gta gca aaa ggc tca Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser aaq qca qqa tat att gac cct att agt gct ttt cag gga caa ctt gaa Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr

210 215 220

gct atc aat cct aaa gaa ttc gtg atg gaa tcc cgc aaa cgc gca agg 720
Ala Ile Asn Pro Lys Glu Phe Val Met Glu Ser Arg Lys Arg Ala Arg
225 230 235 240

cag aca tac acc cgg tac cag act cta gag cta gag aag gag ttt cac 768

Gln Thr Tyr Thr Arg Tyr Gln Thr Leu Glu Leu Glu Lys Glu Phe His

245 250 255

ttc aat cgc tac ttg acc cgt cgg cga agg atc gag atc gcc cac gcc

Phe Asn Arg Tyr Leu Thr Arg Arg Arg Ile Glu Ile Ala His Ala

260 265 270

ctg tgc ctc acg gag cgc cag ata aag att tgg ttc cag aat cgg cgc 864

Leu Cys Leu Thr Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg

275 280 285

atg aag tgg aag aag gag aac tga

Met Lys Trp Lys Lys Glu Asn

290 295

<210> 4

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3APLT: includes ADP-ribosyl transferase C3 (Clostrid
 ium botulinum) and Antennapedia sequence.

<400> 4

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1 5 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 ' 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70

75

80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser

165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr

210 215 220

Ala Ile Asn Pro Lys Glu Phe Val Met Glu Ser Arg Lys Arg Ala Arg
225 230 235 240

Gln Thr Tyr Thr Arg Tyr Gln Thr Leu Glu Leu Glu Lys Glu Phe His 245 250 255

Phe Asn Arg Tyr Leu Thr Arg Arg Arg Ile Glu Ile Ala His Ala
260 265 270

Leu Cys Leu Thr Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg
275 280 285

Met Lys Trp Lys Lys Glu Asn
290 295

<210> 5

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3APS: Includes ADP-ribosyl transferase C3 (Clostrid ium botulinum) and Antennapedia sequence.

<220>

<221> CDS

(1)..(774)<222>

<223>

<400>

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caa aag got tat toa aat act tac cag gag ttt act aat att gat caa 96 Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln

30 25 20

gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa 144 Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys 45 35 40

tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata 192 Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile 60 55 50

aat gga aag cta aga caa aat aag gga gtt atc aat gga ttt cct tca 240 Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 80 70 75 65

aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	
				85					90					95		
												٠				
aag	acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat	336
ГХs	Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	
			100					105					110			
				•												٠
tta	gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att	384
Leu	Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	
		115					120					125				
					٠											
aat	aaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	432
Asn	ГЛS	Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Гуs	Phe	Leu	Asn	Lys	Asp	
	130				•	135					140					
															•	
aga	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtc	tct	caa	480
Arg	Leu	Glu	Tyr	Gly.	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln	
145					150					155					160	
ttt	gca	gga	aga	cca	att	att	aca	caa	ttt	aaa	gta	gca	aaa	ggc	tca	528
Phe	Ala	Gly	Arg	Pro	Ile	Ile	Thr	Gln	Phe	Lys	Val	Ala	Lys	Gly	Ser	•
				165					170					175		
aag	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	cag	gga	caa	ctt	gaa	576
Lys	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Gln	Leu	Glu	
			180					185					190	•		

atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg 624

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu

195 200 205

tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca 672

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr

210 220

gct atc aat cct aaa gaa ttc cgc cag atc aag att tgg ttc cag aat 720
Ala Ile Asn Pro Lys Glu Phe Arg Gln Ile Lys Ile Trp Phe Gln Asn
225 230 235 240

cgt cgc atg aag tgg aag aag gtc gac tcg agc ggc cgc atc gtg act 768

Arg Arg Met Lys Trp Lys Lys Val Asp Ser Ser Gly Arg Ile Val Thr

245 250 255

gac tga 774

Asp

<210> . 6

<211> 257

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3APS: Includes ADP-ribosyl transferase C3 (Clostrid
 ium botulinum) and Antennapedia sequence.

<400> 6

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met

85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile

115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser

165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Arg Gln Ile Lys Ile Trp Phe Gln Asn 225 230 235 240

Arg Arg Met Lys Trp Lys Lys Val Asp Ser Ser Gly Arg Ile Val Thr

245 250 255

Asp

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the amplification of Antennapedia sequenc

<400> 7

gaatcccgca aacgcgcaag gcag

24

<210> 8

<211> 27

<212> DNA

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<213> Artificial Sequence
<220>
<223> Oligonucleotide used in the amplification of Antennapedia sequenc
<400> 8
                                                                    27
teagttetee ttetteeact teatgeg
<210> 9
<211> 54
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide used in the cloning of sequences from Antennapedi
       a
<400> 9
aattccgcca gatcaagatt tggttccaga atcgtcgcat gaagtggaag aagg
                                                                    54
<210> 10
<211> 54
<212> DNA
<213> Artificial Sequence
<220>
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<223> Oligonucleotide used in the cloning of sequences from Antennapedi

<400> 10

ggcggtctag ttctaaacca agctcttagc agcgtagttc accttcttcc agct

54

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used inthe amplification of a sequence correspond ing to amino acid 27-72 of HIV-1 Tat

<400> 11

gaatccaagc atccaggaag tcagcc

26

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used inthe amplification of a sequence correspond ing to amino acid 27-72 of HIV-1 Tat

<400> 12

accagccacc accttctgat a

21

<210> 13

<211> 876

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3-TL: Includes ADP-ribosyl transferase C3 (Clostrid
ium botulinum) and HIV-1 Tat sequence.

<220>

<221> CDS

<222> (1)..(876)

<223>

<400> 13

gga tcc tct aga gtc gac ctg cag gca tgc aat gct tat tcc att aat 48
Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 5 10 15

caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa 96
Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln

20 25 30

gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa 144

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys. 45 35 40 tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata 192 Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile 60 55 50 240 aat gga aag cta aga caa aat aag gga gtt atc aat gga ttt cct tca Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 70 . 80 75 65 288 aat tta ata aaa caa gtt gaa ctt tta gat aaa tct ttt aat aaa atg Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 90 95 85 aag acc cct gaa aat att atg tta ttt aga ggc gac gac cct gct tat 336 Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr 100 105 110 tta gga aca gaa ttt caa aac act ctt ctt aat tca aat ggt aca att 384 Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile 115 120 125 432 aat aaa acg gct ttt gaa aag gct aaa gct aag ttt tta aat aaa gat Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 130 135 140 aga ctt gaa tat gga tat att agt act tca tta atg aat gtc tct caa 480 Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln

145					150					155					160		•
.	gca	~~~			2++	att	202	C22	+++	222	at a	aca	222	aac	tca		528
	_																-
Pne \	Ala	GIÀ	Arg		TTE	тте	THE	GIN		тув	vai	Ala	гу		ser		
				165					170					175			
								•									
aag	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	cag	gga	caa	ctt	gaa		576
Lys	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Gln	Leu	Glu		
	,		180					185					190				
,						•											
atg	ttg	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	atg	aga	ttg		624
Met	Leu	Leu	Pro	Arg	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu		
		195					200					205		•			•
tct	tct	gat	ggt	aaa	caa	ata	ata	att	aca	gca	aca	atg	atg	ggc	aca	•	672
Ser	Ser	Asp	Gly	Lys	Gln	Ile	Ile	Ile	Thr	Ala	Thr	Met	Met	Gly	Thr		
	210					215					220				•		
gct	atc	aat	cct	aaa	gaa	ttc	aaq	cat	cca	gga	agt	caq	cct	aaa	act		720
					Glu									i			
Ala	116	ASII	PIO	пуъ		FIIC	nys	111.5	FIO		DCI	O.I.I.	110	Буб			
225					230					235					240		
gct	tgt _.	acc	aat	tgc	tat	tgt	aaa	aag	tgt	tgc	ttt	cat	tgc	caa	gtt		768
Ala	Cys	Thr	Asn	Cys	Tyr	Cys	ГÀЗ	Lys	Cys	Сув	Phe	His	Cys	Gln	Val		
				245					250					255			
tgt	ttc	ata	aca	aaa	gcc	tta	ggc	atc	tcc	tat	ggc	agg	aag	cgg	aga	•	816
Cys	Phe	Ile	Thr	Lys	Ala	Leu	Gly	Ile	Ser	Tyr	Gly	Arg	Lys	Arg	Arg		
			260					265		•			270			,	

cag cga cga aga gct cat cag aac agt cag act cat caa gct tct cta 864
Gln Arg Arg Arg Ala His Gln Asn Ser Gln Thr His Gln Ala Ser Leu

275 280 285

tca aag cag taa 876

Ser Lys Gln

290

<210> 14

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3-TL: Includes ADP-ribosyl transferase C3 (Clostrid
 ium botulinum) and HIV-1 Tat sequence.

<400> 14

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 5 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 40 45 ·

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 65 70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met

85 90 95

Lys Thr Pro Glu Asn Île Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile

115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp
130 135 140

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln

145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser 165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu
180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Lys His Pro Gly Ser Gln Pro Lys Thr
225 230 235 240

Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln Val

Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Arg Arg 260 265 270

Gln Arg Arg Ala His Gln Asn Ser Gln Thr His Gln Ala Ser Leu
275 280 285

Ser Lys Gln

290

<210> 15

<211> 39

<212> DNA

<213> Artificial Sequence

<220> '

<223> Oligonucleotide used in the cloning of sequences from HIV-1 Tat

<400> 15

aattctatgg tcgtaaaaaa cgtcgtcaac gtcgtcgtg

39

<210> 16

<211> ,39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of sequences from HIV-1 Tat

<400> 16

gataccagca ttttttgcag cagttgcagc agcacagct

39

<210> 17

<211> 756

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3-TS: Includes ADP-ribosyl transferase C3 (Clostrid ium botulinum) and HIV-1 Tat sequence.

<220>

<221> CDS

<222> (1)..(756)

<223>

<400> 17

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Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn
1 10 15

Caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa 96
Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln

20

25

30

gca	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga [.]	cta	agc	aaa		144
Ala	Lys	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	Lỳs		
		35					40					45					
tca	gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata		192
Ser	Glu	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile		
	50					55					60						
aat	gga	aag	cta	aga	çaa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca		240
Asn	Gly	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser		
65					70					75			•		80		
							•										
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg		288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	•	
				85					90					95			
aag	acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat		336
Lys	Thr	Pŗo	Glu	Asn	Ile	Met	Leų	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	,	
			100					105					110				
											•						
tta	gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att		384
Leu	Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	•	
		115					120					125					
aat	aaạ	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat		432
Asn	ГÀг	Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Lys	Phe	Leu	Asn	Lys	Asp		
	130					135					140						•
								•			•						
aga	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtc	tct	caa		480

Arg	Leu	Glu	Туг	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln		
145					150		•	•		155					160		
ttt	gca	gga	aga	cca	att	att	aca	caa	ttt	aaa	gta	gca	aaa	ggc	tca		528
Phe	Ala	Gly	Arg	Pro	Ile	Ile	Thr	Gln	Phe	Lys	Val	Ala	Lys	Gly	Ser		
				165					170			•		175			٠
٠																	
aag	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	cag	gga	caa	ctt	gaa		576
Lys	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Gln	Leu	Glu .	•	
			180	•			•	185					190		•		
atg	ttg	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	atg	aga	ttg		624
Met	Leu	Leu	Pro	Arg	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu		
		195				•	200					205					
		195				•	200					205					
tct	tct		ggt	aaa	caa	ata		att	aca	gca	aca		atg	ggc	aca		672
	tct Ser	gat					ata					atg					672
		gat					ata					atg					672
	Ser	gat				Ile	ata				Thr	atg					672
Ser	Ser	gat Asp	Gly	Lys	Gln	Ile 215	ata Ile	Ile	Thr	Ala	Thr 220	atg Met	Met	Gly	Thr		720
Ser gct	Ser 210	gat Asp aat	Gly	Lys	Gln gaa	Ile 215 ttc	ata Ile tat	Ile	Thr	Ala	Thr 220	atg Met	Met	Gly	Thr		
Ser gct	Ser 210 atc	gat Asp aat	Gly	Lys	Gln gaa	Ile 215 ttc	ata Ile tat	Ile	Thr	Ala	Thr 220	atg Met	Met	Gly	Thr		
Ser gct	Ser 210 atc	gat Asp aat	Gly	Lys	Gln gaa Glu	Ile 215 ttc	ata Ile tat	Ile	Thr	Ala aaa Lys	Thr 220	atg Met	Met	Gly	Thr cgt Arg		
Ser gct Ala 225	Ser 210 atc	gat Asp aat Asn	Gly cct Pro	Lys aaa Lys	gaa Glu 230	Ile 215 ttc Phe	ata Ile tat Tyr	ggt	Thr gct Ala	aaa Lys 235	Thr 220 aaa Lys	atg Met cgt Arg	Met	Gly	Thr cgt Arg		
Ser gct Ala 225	ser 210 atc Ile	gat Asp aat Asn	Gly cct Pro	Lys aaa Lys tcg	gaa Glu 230	Ile 215 ttc Phe	ata Ile tat Tyr	ggt Gly	Thr gct Ala	aaa Lys 235	Thr 220 aaa Lys	atg Met cgt Arg	Met	Gly	Thr cgt Arg		720

<210> 18

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3-TS: Includes ADP-ribosyl transferase C3 (Clostrid ium botulinum) and HIV-1 Tat sequence.

<400> 18

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 5 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser
165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190

Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Tyr Gly Ala Lys Lys Arg Arg Gln Arg
225 230 235 240

Arg Arg Val Asp Ser Ser Gly Pro His Arg Asp
245 250

<210> 19

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> Includes GST sequences, ADP-ribosyl transferase C3 (C. botulinum
) sequence and a random basic amino acid sequence.

<220>

<221> CDS

<222> (1)..(1413)

<223>

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Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro		
1	·			5					10					15			
					•												
act	cga	ctt	ctt	ttg	gaa	tat	ctt	gaa	gaa	aaa	tat	gaa	gag	cat	ttg	96	5
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu		
			20					25					30				
tat	gag	cgc	gat	gaa	ggt	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg	144	4
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
		35					40					45					
ggt	ttg	gag	ttt	ccc	aat	ctt	cct	tat	tat	att	gat	ggt	gat	gtt	aaa	19:	2
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	ГÀа		
	50					55					60						
															·		
tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tat	ata	gct	gac	aag	cac	aac	24	0
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
65					70			٠		75					80		
							•	•									
atg	ttg	ggt	ggt	tgt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa	28	8
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
		÷		85					90					95			
										•							
gga	gcg	gtt	ttg	gat	att	aga	tac	ggt	gtt	tcg	aga	att	gca	tat	agt	33	6
Gly	Ala	۷al	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		

100 105 110

aaa	gac	ttt	gaa	act	ctc	aaa	gtt.	gat	ttt	ctt	agc	aag	cta	cct	gaa		384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Гуs	Leu	Pro	Glu		
		115					120				٠	125					
															,		
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat		432
Met	Leu	Lys	Met	Phe	Clu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
	130					135					140						
ggt	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat		480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
145					150					155					160		
			•														
gtt	gtt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	tta	-	528
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu-	Asp	Ala	Phe	Pro	Lys	Leu		٠
÷				165		٠			170					175			
						•									•		
gtt	tgt	ttt	aaa	aaa	cgt	att	gaa	ąct	atc	cca	caa	att	gat	aag	tac	•	576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180		•			185					190				
																	•
ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	gcc	•	624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195					200					205					
acg	ttt	ggt	ggt	ggc	gac	cat	cçt	cca	aaa	tcg	gat	ctg	gtt	ccg	cgt		672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		_
	210					215					220						-

gga	tcc	tct	aga	gtc	gac	ctg	cag	gca	tgc	aat	ġct	tat	tcc	att	aat		720
Gly	Ser	Ser	Arg	Val	Asp	Leu	Gln	Ala	Cys	Asn	Ala	Tyr	Ser	Ile	Asn		
225					230					235					240		
•						÷											
caa	aag	gct	tat	tca	aat	act	tac	cag	gag	ttt	act	aat	att	gat	caa		768
Gln	Lys	Ala	Tyr	Ser	Asn	Thr	Tyr	Gln	Glu	Phe	Thr	Asn	Ile	qaA	Gln		
				245					250					255			
gca	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa		8:16
Ala	Lys	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	ГÀЗ		
			260		• ,	٠		265		•			270				
		•				, .											
tca	gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata		864
Ser	Glu	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile		
		275	٠				280					285					
			cta				•										912
Asn		Lys	Leu	Arg	Gl'n	Asn	ГЛЗ	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser		
	290	,				295					300						
								•									•
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg		960
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	ГЛЗ	Ser	Phe	Asn	Lys	Met		
305					310					315					320		
_			gaa]	8000
Ьуs	Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr		
				325					330					335			

								•								
tta	gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att	1056
Leu	Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Àsn	Gly	Thr	Ile	
			340		٠			345					350			
aat	aaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	1104
Asn	Lys	Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Lys	Phe	Leu	Asn	Lys	Asp	
		355					360					365		•		
															•	
aga	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtt	tct	caa	1152
Arg	Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	·Gln	٠
	370					375			•		380					
						•										
ttt	qca	qqa	aga	cca	att	att	aca	aaa	ttt	aaa	gta	gca	aaa	. ggc	tca	1200
	_		Arg						-							
.385		_			390					395					400	
aag	aca	gga	tat	att	gac	cct	att	agt	qct	ttt	cag	gga	caa	ctt	gaa	1248
			Tyr													
- <i>y</i> -		1	-1-	405					410			_		415		
				100							·.				•	
a b a		a++	cct	202	ast	aat	act	tat	cat	ata	aac	gat	ato	aga	tta	1296
			Pro													
Mec.	ьeu	Leu			ura	per	1111	425		J. J. C.	nsp	nop	430			
			420					423					1 50			
												_ 1				1244
			ggt													1344
Ser	Ser	Asp	Gly	. PAs	Gln	. Ile	Ile	: Ile	Thr	Ala	Thr			: GIY	Thr	
		435			•		440	•				445	i			
gct	ato	aat	cct	aaa	gaa	ttc	aga	agg	aaa	caa	aga	aga	aaa	aga	aga	1392

PCT/CA2004/001763 WO 2005/030248

Ala Ile Asn Pro Lys Glu Phe Arg Arg Lys Gln Arg Arg Lys Arg Arg 455 460 450

ctg cag gcg gcc gca tcg tga

1413 .

Leu Gln Ala Ala Ser

470 465

20 <210>

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Includes GST sequences, ADP-ribosyl transferase C3 (C. botulinum) sequence and a random basic amino acid sequence.

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35

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro 15 1 . 5 10

Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 30 20 25

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 45

40

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser

100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp

145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr

180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn 225 230 235 240

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
245 250 255

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

260 265 270

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
275 280 285

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser
290 295 300

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 305 310 315 320

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

325 330 335

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile

340 345 350

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp
355 360 365

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
370 375 380

Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser

385 390 395 400

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu
405 410 415

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
420 425 430

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
435 440 445

Ala Ile Asn Pro Lys Glu Phe Arg Arg Lys Gln Arg Arg Lys Arg Arg 450 455 460

Leu Gln Ala Ala Ala Ser 465 470

<210> 21

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Random basic amino acid sequence of C3Basic1

<400> 21

Lys Arg Arg Arg Arg Pro Lys Lys Arg Arg Arg Ala Lys Arg Arg

1 5 10 15

<210> 22

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of a random basic amino acid sequence in C3Basic1

<400> 22

aagagaaggc gaagaagacc taagaagaga cgaagggcga agaggaga

48

<210> 23

<211> 48

<212> DNA.

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of a random basic amino acid sequence in G3Basic1

PCT/CA2004/001763

WO 2005/030248

<400> 23

ttctcttccg cttcttctgg attcttctct gcttcccgct tctcctct

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<210> 24

<211> 792

DNA <212>

Artificial Sequence ·<213>

<220>

Sequence of C3Basic1: includes ADP-ribosyl transferase C3 (Clost <223> ridium botulinum) sequence and a sequence encoding a random basic amino acid sequence and a Histidine tag.

<220>

<221> CDS

(1).:(792) <222>

<223>

<400> 24

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96 caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln

> 30 20 25

gca	aaa	gct	tgg	ggt _.	aat	gcţ	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	144
Ala	Lys	Ala	Trp	Gly	Asņ	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	Lys	
		35					40					45				
tca	gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata	192
0	a 3	T	a1.,	מ מ	TTA		Cor	Фт.	ጥኮኦ	Laze	Cor	פות	Car	Glu	Tle	
ser		гÀг	GIU	Ата	Ile		ser	ıyı	1111	пув		ALA	PCI	GIU	116	
	50					55					60					
										_ •	•				.	240
					caa	•										240
Asn	Gly	ГÀЗ	Leu	Arg		Asn	Lys	GTA	Val		Asn	GIÀ	Pne	Pro	Ser	
65					70		٠			75	٠				80	
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	
٠				85					90					95		
		•	•													
aag	acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat	336
Lys	Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp ·	Pro	Ala	Tyr	
			100				•	105					110			
tta	gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	·att	384
Leu	Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	
	-	115	•	•			120					125	•			
aat	aaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	432
Asn	Ьуs	Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Lys	Phe	Leu	Asn	. Lys	Asp	
	130					135					140					

aga	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtt	tct	caa	48	0
Arg	Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln		
145					150					155					160		
ttt	gca	gga	aga	cca	att	att	aca	aaa	ttt	aaa	gta	gca	aaa	ggc	tca	52	8
Phe	Alá	Gly	Arg	Pro	Ile	Ile	Thr	ьуs	Phe	Lys	Val	Ala	ГÀЗ	Gly	Ser	•	
				165					170					175		•	
aag	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	cag	gga	caa	ctt	gaa	57	6
Lys	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Gln	Leu	Glu		
•	•		180					185				•	190				
																•	
	_			-	cat	_									•	62	4
Met	Leu		Pro	Arg	His	Ser		Tyr	His	Ile	Asp		Met	Arg	Leu		
		195					200					205					
t- a-t-	+	~~ +	~~+		caa	2+2	2+2	~++	202	aca		ato	ata	aac	aca	67	12
		_			Gln											0,	۵.
, JCI	210	nop	O _T		0	215					220			1		•	
gct	atc	aat	cct	aaa	gaa	ttc	aag	aga	agg	cga	aga	aga	cct	aag	aag	72	0
Ala	Ile	Asn	Pro	Lys	Glu	Phe	Lys	Arg	Arg	Arg	Arg	Arg	Pro	Ьуs	Lys		
225					230					235					240		
						•							•				
aga	cga	agg	gcg	aag	agg	aga	cac	cac	cac	cac	cac	cac	gtc	gac	tcg	76	8
Arg	Arg	Arg	Ala	Ļys	Arg	Arg	His	His	His	His	His	His	Val	Asp	Ser		
				245					250					255			

agc ggc cgc atc gtg act gac tga

·792

Ser Gly Arg Ile Val Thr Asp

260

<210> 25

<211> 263

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3Basic1: includes ADP-ribosyl transferase C3 (Clost ridium botulinum) sequence and a sequence encoding a random basic amino acid sequence and a Histidine tag.

<400> 25

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 5 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile

50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110 ...

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser 165 170 175 Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Lys Arg Arg Arg Arg Pro Lys Lys
225 230 235 240

Arg Arg Arg Ala Lys Arg Arg His His His His His Val Asp Ser

Ser Gly Arg Ile Val Thr Asp

<210> 26

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Random amino acid sequence of C3Basic2

<400> 26

Lys Arg Arg Arg Lys Lys Arg Arg Gln Arg Arg Arg

1 5 10

<210> 27

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of a random basic amino acid sequence in C3Basic2

<400> 27

aagcgtcgac gtagaaagaa acgtagacag cgtagacgt

39

<210> 28

<211> 39

<212> DNA

<213> Artificial Sequence

<220> .

<223> Oligonucleotide used in the cloning of a random basic amino acid sequence in C3Basic2

<400> 28

ttcgcagctg catctttctt tgcatctgtc gcatctgca

39

<210> 29

<211> 783

<212> DNA

<213> Artificial Sequence

<220> -

<223> Sequence of C3Basic2: includes sequences from ADP-ribosyl-transf erase C3 (Clostridium botulinum) and a sequence encoding a random basic amino acid sequence and a histidine tag.

.<220>

<221> CDS

<222> (1)..(783)

<223>

<400> 29

gga tcc tct aga gtc gac ctg cag gca tgc aat gct tat tcc att aat
Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

10

15

caa	aag	gct	tat	tca	aat	act	tac	cag	gag	ttt	act	aat	att	gat	caa		96
Gln	Lys	Ala	Tyr	Ser	Asn	Thr	Tyr	Gln	Glu	Phe	Thr	Asn	Ile	Asp	Gln		
			20					25			٠		30				
										·							
gca	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa		144
Ala	Lys	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	ŗys		
		35					40	•				45					
															į.		
tca	gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	ågt	gaa	ata		192
Ser	Glú	Гуs	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile		
	50					55					60					•	
										·							
aat	gga	aag	cta	aga	caa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca		240
Asn	Gly	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser		
65.					70				·	75					80		
													•			•	
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	•	288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	ГЛЗ	Ser	Phe	Asn	Lys	Met		
				85					90					95			
				•													
aag	acc	cct	gaa	aat	att	, atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat		336
					Ile												
			100					105					110				
•																	
tta	qqa	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	atť		384
					Gln												
	-	115					120					125	-				
						٠											•
aat.	aaa	aco	act	ttt	gaa	aao	get	aaa	gct	aaσ	ttt	tta	aat	aaa	gat		432
,	aud	~~9	300		544	~~9	500		500	~~3					_~~		

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp aga ctt gaa tat gga tat att agt act tca tta atg aat gtt tct caa Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln ttt gca gga aga cca att att aca aaa ttt aaa gta gca aaa ggc tca Phe Ala Gly Arg Pro Ile Thr Lys Phe Lys Val Ala Lys Gly Ser aag gca gga tat att gac cct att agt gct ttt cag gga caa ctt gaa Lys Ala Gly Tyr Ile Asp Pro Ile' Ser Ala Phe Gln Gly Gln Leu Glu atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr gct atc aat cct aaa gaa ttc aag cgt cga cgt aga aag aaa cgt aga Ala Ile Asn Pro Lys Glu Phe Lys Arg Arg Arg Lys Lys Arg Arg cag cgt aga cgt cac cac cac cac cac gtc gac tcg agc ggc cgc Gln Arg Arg Arg His His His His His Val Asp Ser Ser Gly Arg

245 250 255

atc gtg act gac tga . 783

Ile Val Thr Asp

260

<210> 30

<211> 260

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3Basic2: includes sequences from ADP-ribosyl-transf erase C3 (Clostridium botulinum) and a sequence encoding a random basic amino acid sequence and a histidine tag.

<400> 30

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 5 10 15.

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 130 135 140

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Lys Arg Arg Arg Arg Lys Lys Arg Arg 225 230 235 240

Gln Arg Arg Arg His His His His His Val Asp Ser Ser Gly Arg

245 250 255

Ile Val Thr Asp

260

<210> 31 <211> 9 <212> PRT <213> Artificial Sequence <220> <223> Reverse HIV-1 Tat amino acid sequence of C3Basic3 <400> 31 Arg Arg Lys Gln Arg Arg Lys Arg Arg 5 · 1 <210> 32 <211> 27 <212> DNA <213> Artificial Sequence <220> <223> Oligonucleotide used in the cloning of a reverse HIV Tat sequence . in C3Basic3 <400> 32 27 agaaggaaac aaagaagaaa aagaaga

<211> 27

<210> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of a reverse HIV Tat sequence in C3Basic3

<400> 33

tcttcctttg tttcttcttt ttcttct

27

<210> 34

<211> 771

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3Basic3: includes sequences from ADP-ribosyl tranfer ase C3 (C. botulinum) and a sequence encoding a reverse HIV-1 Tat amino acid sequence and a Histidine tag

<220>

<221> CDS

<222> (1)..(771)

<223>

<400> 34

gga tcc tct aga gtc gac ctg cag gca tgc aat gct tat tcc att aat

48

Gly	Ser	Ser	Arg	Val	Asp	Leu	Gln	Ala	Cys	Asn	Ala	Tyr	Ser	Ile	Asn ,	->
1.				5					10					15		
caa.	aag	gct	tat	tca	aat	act	tac	cag	gag	ttt	act	aat	att	gat	caa	96
Gln	Ьуs	Ala	Tyr	Ser	Asn	Thr	Tyr	Gln	Glu	Phe	Thr	Asn	Ile	Asp	Gln	
			20					25					30			1
				•												
gca	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	144
Ala	Lys	Ala	Trp	Glу	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	ГÀЗ	
		35					40					45				
																•
tca	gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata	192
Ser	Glu	rys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile	
	50					55					60	•				
													•		•	
aat	gga	aag	cta	aga	caa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca	240
Asn	Gly	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	
65					70					75					80	
									·							
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	
٠				85					90			,	•	95		
															•	
aag	acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat	336
Lys	Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	
			100					105					110		٠	•
•																
			•				act								_	384
Leu	Glv	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Glv	Thr	Ile	

115 120 125

aat	aaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	432
Asn	rys.	Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Lys	Phe	Leu	Asn	Lys	Asp	
	130					135				•	140					
aga	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtt	tct	caa	480
Arg	Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln	
145					150					155			•		160	
ttt	gca	gga	aga	cca	att	att	aca	aaa	ttt	aaa	gta	gca	aaa	ggc	tca	528
Phe	Ala	Gly	Arg	Pro	İle	Ile	Thr	Lys	Phe	Lys	Val	Ala	Lys	Gly	Ser	
		٠		165					170					175		
									•							
aag	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	cag	gga	caa	ctt	gaa	576
Lys	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Gln	Leu	Glu	
			180	•				185	•				190			•
										•						
atg	ttg	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	atg	aga	ttg	624
									His							
		195		٦			200	-			-	205	•			
				•												
tat	tat	ast	aat	222	Caa	ata	ata	2++	aca		aca	ato	ata	aac	aca	672
						-										
ser		Ąsp	GIĀ	гÀг	GIII		TTE	TIG	Thr	Ата		Mec	Mec	GIY	1111	
	210					215					220					
		•														
					_				aaa							720
Ala	Ile	Asn	Pro	Lys	Glu	Phe	Arg	Arg	Lys	Gln	Arg	Arg	Lys	Arg	Arg	
225				. `	230					235					240	

Cac cac cac cac cac gtc gac tcg agc ggc cgc atc gtg act gac 768

His His His His His Val Asp Ser Ser Gly Arg Ile Val Thr Asp

245

250

255

tga 771

<210> 35

<211> 256

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3Basic3: includes sequences from ADP-ribosyl tranfer ase C3 (C. botulinum) and a sequence encoding a reverse HIV-1 Tat amino acid sequence and a Histidine tag

<400> 35

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 5 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met

85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp
130 135 140

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser

165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu
180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Arg Arg Lys Gln Arg Arg Lys Arg Arg 225 230 235 240

His His His His His Val Asp Ser Ser Gly Arg Ile Val Thr Asp

245 250 255

<210> 36

<211> 887

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3APLT: includes sequences from ADP-ribosyl transfer ase C3 (Clostridium botulinum) and a sequence encoding a proline rich region.

<220>

<221> CDS

<222> (1)..(747)

<223>

<400> 36

gga tcc tct aga gtc gac ctg cag gca tgc aat gct tat tcc att aat 48
Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn
1 5 10 15

caa aag gct tat tca aat áct tac cag gag ttt act aat att gat caa 96

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln

20 25 30

gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa 144
Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys
35 40 45

tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata 192 Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile

50 55 60

aat	gga	aag	cta	aga	caa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca		240
Asn	σΙу	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser		
65			•		70					75					80		
													•				٠.
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg		288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	ГÀа	Met		
				85					90					95			•
									•								
aag	acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat		336
Lys	Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	qaA	Pro	Ala	Tyr		
			100					105					110				
tta	gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att	٠	384
Leu	Gly	Thr	Glu	Phe	Gln	Asn ·	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	•	
		115					120					125					
												٠					
aat	aaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat		432
Asn	Lys	Thr	Ala	Phe	Glu	ГÀЗ	Ala	Lys	Ala	Lys	Phe	Leu	Asn	Lys	Asp		
	130					135					140						
aga	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtt	tct	caa		480
Arg	Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln		
145					150	•				155					160		
			`														
٠	-														tca		528
Phe	Ala	Gly	Arg	Pro	Ile	Ile	Thr	Lys	Phe	Lys	Val	Ala	ГÀЗ	Gly	Ser		
				165					170					175			

Lys Ala Gly Tyr 1le Asp Pro 1le Ser Ala Phe Ala Gly Glu Leu Glu atg ttg t	624
atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 205 tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr	624
Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 205 tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr	624
Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 205 tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr	624
tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr	
tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr	
Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr	
Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr	
	672
210 215 220	
gct atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc	· 720
Ala Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly	· .
225 230 235 240	
•	
aga cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac	767
Arg His Thr Pro Gly Thr Arg Leu	
245	
ttcaatcgct acttgacccg tcggcgaagg atcgagatcg cccacgccct gtgcctcac	g 827
gagcgccaga taaagatttg gttccagaat cggcgcatga agtggaagaa ggagaactg	ga 887
<210> 37	
<211> 248	
<212> PRT <213> Artificial Sequence	

<220>

<223> Sequence of C3APLT: includes sequences from ADP-ribosyl transfer ase C3 (Clostridium botulinum) and a sequence encoding a proline rich region.

<400> 37

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 5 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met

90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser 165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu 180 185 190

Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly
225 230 235 240

Arg His Thr Pro Gly Thr Arg Leu

245

<210> 38

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of C3APLT in pET vector

<400> 38

ggatctggtt ccgcgtcata tgtctagagt'cgacctg

37

. <210> 39

<211> 32

<212> DNA

	• •	
<213>	Artificial Sequence	
<220>		
<223>	Oligonucleotide used in the cloning of C3APLT in pET vector	
<400>	39	
cgcgga	tcca ttagttctcc ttcttccact tc	32
<210>	40	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Oligonucleotide used in the sequencing of C3APLT	
	·	
<400>	4 Ò	
aaatta	aatac gactcactat aggg	24
<210>	41	
<211>	19	•
<212>	DNA	
<213>	Artificial Sequence	
· <220>		
	Oligonucleotide used in the sequencing of C3APLT	

<400> 41

gctagttatt gctcagcgg

1.9

<210> 42

<211> 888

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3APLT in a pET vector: includes sequences from ADP.
 -ribosyl transferase C3 (Clostridium botulinum) and a sequence en
 coding a proline rich region.

<220>

<221> CDS

<222> (1)...(744)

<223>

<400> 42

atg tot aga gto gca ctg cag gca tgc aat gct tat too att aat caa 48
Met Ser Arg Val Ala Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn Gln

1 5 10 15

aag gct tat tca aat act tac cag gag ttt act aat att gat caa gca 96
Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala

20 25 30

aaa	gct	tigg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	tca		144
Lys	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	Lys	Ser	-	
		35					40					45					,
				•				٠									
gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata	aat		192
Glu	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ïle	Asn		
	50					55					60						
•																	
gga	aag	cta	aga	caa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca	aat		240
Gly	ГЛЗ	Leu	Arg	Gln	Asn	гуs	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	Asn		
65					70					75			•		80		
										•							
tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	aag		288
Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	Lys		
				85					90					95			
						-											
acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat	tta		336
Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	Leu		
			100					105					110		•		
		•															
gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att	aat		384
Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	Asn		
		115					120					125					
•				•			٠			•							
aaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	aga	•	432
Гуs	Thr	Ala	Phe	Glu	Lys	Ala	Ŀÿs	Ala	Lys	Phe	Leu	Asn	Lys	Asp	Arg		
	130					135					.140						

cţt	gaa	tat	gga	tat	att	agt	act	tca	tta _.	atg	aat	gtt	tct	caa	ttt	480	ı
Leu	Gľu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln	Phe		
145					150					155					160		
														•		-	
aa.	aa s		CCS	att	att	aca	222	ttt	aaa	αta	gca	ааа	, aac	tca	aaq	528	3
_		•	•					Phe				•		-			
ATA	GLY	nrg	110	165	110		Lyb		170			_, _	2	175	-3-		
				103					1,0								
~~~	~~·	tat	a++	as c	cct	2++	agt	gct	+++	aca	aga	саа	ctt	gaa	ato	576	á
								Ala									
AIA	Gry	-7-	180	Hop	110	110	501	185	- 110		<i>9-1</i>		190				
			100														
tta	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	ato	aga	tta	tct	624	4
								His									
пец	пец	195	Arg	1113	DCI		200		110	ше	ш	205	5				
		193					200									÷	
i at	ast	aat	222	caa	a. ta	ata	att	aca	gca	aca	ato	ato	aac	aca	act	672	2
•								Thr									
DCI	210	CLY	ביינב	0411	110	215					220		2				
	210	•				222											
atc	aat	cct	222	caa	ttc	ata	ato	aat	aaa	gca	i. aac	aca	caa	aac	aga	720	o
			•					Asn									
225	ASII	PIO	цув	GIU	230	Val	MCC	71011	110	235			Can	027	240		
223					250					233							
<b>a</b> >+	2.55		aa+	200	200	ata	tac	acc	tage	നമമ	aasa ,	tttc	ac t	tcaa	tcgct	77-	۵
								age	caya	<b>3</b> aa	3263		<b>40</b> 0	Jua	22300	, ,	_
HIS	inr	PIO	GTĀ			Leu					,						
				245		•											

acttgacccg tcggcgaagg atcgagatcg cccacgccct gtgcctcacg gagcgccaga

PCT/CA2004/001763 WO 2005/030248

taaagatttg gttccagaat cggcgcatga agtggaagaa ggaggactaa ctga

888

<210> 43

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3APLT in a pET vector: includes sequences from ADP -ribosyl transferase C3 (Clostridium botulinum) and a sequence en coding a proline rich region.

<400> 43

Met Ser Arg Val Ala Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn Gln 15 10 1

Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala 30 20 25

Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser 40 45 35

Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn

50 55 60

Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn 65 70 . 75 80

Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys

85 90 95

Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu

100 105 110

Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn
115 . 120 . 125

Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg

130 135 140

Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe

145 150 155 160

Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys

165 170 175

Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met
180 185 190

Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser

195 200 205

Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala
210 215 220

Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg
225 230 235 240

His Thr Pro Gly Thr Arg Leu

245

<210> 44

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of Antennapedia from C3APL

<400> 44

Val Met Glu Ser Arg Lys Arg Ala Arg Gln Thr Tyr Thr Arg Tyr Gln

1 5 10 15

Thr Leu Glu Leu Glu Lys Glu Phe His Phe Asn Arg Tyr Leu Thr Arg

Arg Arg Ile Glu Ile Ala His Ala Leu Cys Leu Thr Glu Arg Gln
35 40 45

Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Glu Asn 50 55 60

<210> 45

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of Antennapedia from C3APS

<400> 45

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys

1 5 10 15

Val Asp Ser

<210> 46

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of HIV-1 Tat from C3-TL

<400> 46

Lys His Pro Gly Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys

1 5 10 15

Lys Lys Cys Cys Phe His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu
20 25 30

Gly Ile Ser Tyr Gly Arg Lys Arg Arg Gln Arg Arg Arg Ala His Gln
35 40 45

Asn Ser Gln Thr His Gln Ala Ser Leu Ser Lys Gln

50 55 60

<210> 47

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of HIV-1 Tat from C3-TS

<400> 47

Tyr Gly Ala Lys Lys Arg Arg Glm Arg Arg Arg Val Asp Ser Ser Gly

15

1 5 10

Pro His Arg Asp

20

<210> 48

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the proline rich region of C3APLT

<400> 48

Val Met Asn Pro Ala Asn Ala Gln Gly Arg His Thr Pro Gly Thr Arg

1 5 10 15

Leu

<210> 49

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence fused to C3 protein to created C3 Tat-short

<400> 49

Tyr Gly Arg Lys Arg Arg Gln Arg Arg Arg

10

<210> 50

<211> 8

<212> PRT

<213> Artificial Sequence

<220> <223> Reverse sequence of Tat amino acids fused to C3 protein to created C3Basic3 <400> 50 Arg Arg Gln Arg Arg Lys Lys Arg 1 <210> 51 <211> 12 <212> PRT <213> Artificial Sequence <220> <223> transport peptide rich in Proline <400> 51 Ala Ala Val Leu Leu Pro Val Leu Leu Ala Ala Pro . 5 10

<210> 52

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Sperm fertiline alpha peptide

<400> 52

His Pro Ile Gln Ile Ala Ala Phe Leu Ala Arg Ile Pro Pro Ile Ser

1 5 10 15

Ser Ile Gly Thr Cys Ile Leu Lys

20

<210> 53.

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence from the C3Basic3

<400> 53

Arg Arg Lys Gln Arg Arg Lys Arg Arg

1

<210> 54

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3-07Q189A

<400> 54

atgtctagag tcgacctgca ggcatgcaat gcttattcca ttaatcaaaa ggcttattca 60 aatacttacc aggagtttac taatattgat caagcaaaag cttggggtaa tgctcagtat 120 aaaaagtatg gactaagcaa atcagaaaaa gaagctatag tatcatatac taaaagcgct 180 agtgaaataa atggaaaget aagacaaaat aagggagtta tcaatggatt teettcaaat 240 ttaataaaac aagttgaact tttagataaa tettttaata aaatgaagac eeetgaaaat .300 attatgttat ttagaggcga cgaccctgct tatttaggaa cagaatttca aaacactctt 360 cttaattcaa atggtacaat taataaaacg gcttttgaaa aggctaaagc taagttttta 420 aataaagata gacttgaata tggatatatt agtacttcat taatgaatgt ttctcaattt 480 gcaggaagac caattattac aaaatttaaa gtagcaaaag gctcaaaggc aggatatatt 540 gaccetatta gtgettttgc aggageaett gaaatgttge tteetagaea tagtaettat 600 catatagacg atatgagatt gtcttctgat ggtaaacaaa taataattac agcaacaatg 660 atgggcacag ctatcaatcc taaagaattc gtgatgaatc ccgcaaacgc gcaaggcaga 720 catacacccg gtaccagact ctag 744.

<210> 55

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

.<223> Amino acid sequence of C3-07Q189A

/															
<400	)> 5	55													
Met	Ser	Arg	Val	Asp	Leu	Gln	Ala	Cys	Asn	Ala	Týr	Ser	Ile	Asn	Glr
1				5					10					15	
ГÀв.	Ala	Tyr	Ser	Asn	Thr	Tyr	Gln	Glu	Phe	Thr	Asn	Ile	Asp	Gln	Ala
			20 ·			÷		25					30		
ГЛЗ	Ala	Trp	GlÀ	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	Lys	Sei
		35					40					45		÷	
Glu	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile	Ası
	50					55					60				
Gly	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	Ası
65					70					75					80
Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	ьys
				85		•			90					95	
Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	Let
			100					105					110		
Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	Ası
		115			٠		120				•	125			
ГХа	Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Lys	Phe	Leu	Asn	Lys	Asp	Arg
	130					135					140			_	
Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	ser	Gln	Ph
145					150					155			•		16
Ala	Gly	Arg	Pro	Ile	Ile	Thr	Gln	Phe	Lys	Val	Ala	Lys	Gly	Ser	Ľу
•				165					170					175	٠
Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Ala	Leu	Glu	Me
			180					185					190	•	٠
Leu	Leu	Pro	Arg	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu	Se
		105					200					205			

235

240

Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220

Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225

His Thr Pro Gly Thr Arg Leu

245

230

<210> 56

<211> 783

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of BA-05

<400> 56

ggatcctcta gagtcgacct gcaggcatgc aatgcttatt ccattaatca aaaggcttat 60 tcaaatactt accaggagtt tactaatatt gatcaagcaa aagcttgggg taatgctcag 120 tataaaaagt atggactaag caaatcagaa aaagaagcta tagtatcata tactaaaagc 180 gctagtgaaa taaatggaaa gctaagacaa aataagggag ttatcaatgg atttccttca 240 aatttaataa aacaagttga acttttagat aaatctttta ataaaatgaa gacccctgaa 300 aatattatgt tatttagagg cgacgaccct gcttatttag gaacagaatt tcaaaacact 360 cttcttaatt caaatggtac aattaataaa acggcttttg aaaaggctaa agctaagttt 420 ttaaataaag atagacttga atatggatat attagtactt cattaatgaa tgtttctcaa 480 tttgcaggaa gaccaattat tacaaaattt aaagtagcaa aaggctcaaa ggcaggatat 540 attgacccta ttagtgcttt tgcaggacaa cttgaaatgt tgcttcctag acatagtact 600 tatcatatag acgatatgag attgtcttct gatggtaaac aaataataat tacagcaaca 660

720

780

783

atgatgggca	cagctatcaa	tcctaaagaa t	tcgtgatga at	cccgcaaa	cgcgcaaggc						
agacatacac ceggtaccag actetagage tagagaagga gtttcactte aategeta											
tga											
		•			•						
<210> 57		•									
<211> 247	247										
<212> PRT	> PRT										
<213> Artificial Sequence											
<220>											
<223> Amino acid sequence of pET9a-BA-07											
<400> 57			•								
Met Ser Ar	g Val Asp L	eu Gln Ala Cy	rs Asn Ala Ty	r Ser Ile	Asn Gln						
1	5		10		15						
Lys Ala Ty	r Ser Asn T	hr Tyr Gln Gl	u Phe Thr As	n Ile Asp	Gln Ala						
	20	, 25	5	30							
Lys Ala Tr	p Gly Asn A	la Gln Tyŕ Ly	vs Lys Tyr Gl	y Leu Ser	Lys Ser						
35		40		45							
Glu Lys Gl	u Ala Ile V	al Ser Tyr Th	ır Lys Ser Al	a Ser Gļu	Ile Asn						
50		55	. 60								
Gly Lys Le	u Arg Gln A	an Lys Gly Va	l lle Asn Gl	y Phe Pro	Ser Asn						
65	7(	)	75		, 80						
Leu Ile Ly	s Gln Val G	lu Leu Leu As	p Lys Ser Ph	e Asn Lys	Met Lys						
	85		90		95						
Thr Pro Gl	u Asn Ile Me	et Leu Phe Ar	g Gly Asp As	p Pro Ala	Tyr Leu						
	100	10	5	110	•						

Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn

115 120 125

Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg

130 135 140

Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe

145 150 155 160

Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys

. 165 170 175

Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met

Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser

195 . 200 205

Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala

210 · 215 220

Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg

225 230 235 240

His Thr Pro Gly Thr Arg Leu

245

<210> 58

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> .58

cctaaagaat tcgtgatgaa tcccgcaaac gcgca

<210> 59

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 59

tgcgcgtttg cgggattcat cacgaattct ttagg

35